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The lack of comparable metabolic state assays severely limits understanding the metabolic changes caused by genetic or environmental perturbations. The present study reports the application of a novel derivatization method for metabolome analysis of yeast, coupled to data-mining software that achieve comparable throughput, effort and cost compared with DNA arrays. Our sample workup method enables simultaneous metabolite measurements throughout central carbon metabolism and amino acid biosynthesis, using a standard GC-MS platform that was optimized for this purpose. As an implementation proof-of-concept, we assayed metabolite levels in two yeast strains and two different environmental conditions in the context of metabolic pathway reconstruction. We demonstrate that these differential metabolite level data distinguish among sample types, such as typical metabolic fingerprinting or footprinting. More importantly, we demonstrate that this differential metabolite level data provides insight into specific metabolic pathways and lays the groundwork for integrated transcription-metabolism studies of yeasts.

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